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REMARKS

Claims 1-12 are pending in this application.

Regarding the sequence listing, nucleotides 185 to 1114 of SEQ ID NO:8 encode the 310 amino acid sequence of SEQ ID NO:9.

Applicants thank the Examiner for and acknowledge receipt of the initialed IDS.

The Brief Description of the Drawings at page 4, line 22 has been amended, at the Examiner's request, to better correlate the description with the figures. No new matter is believed to have been added.

Claims 1-3 and 6-12 were rejected under 35 U.S.C. §112, first paragraph, as failing to comply with the written description requirement. It is stated at the bottom of page 2 bridging page 3 that "[t]he claims reciting 85-90% sequence identity lack adequate written description because Applicant does not disclose a representative number of species as encompassed by these claims." It is respectfully submitted that Applicant does disclose to one of ordinary skill in the art a representative number of pantothenate synthetases with at least 85% sequence identity to SEQ ID NO:9.

Applicants kindly invite the Examiner's attention to Genschel, U. et al. (1999) Biochem J. 341:669-678 ["Genschel"] which describes two plant genes encoding functional pantothenate synthase ("PS") from rice and lotus. (Specification, page 1 at lines 17-18). Specifically, Genschel describes the isolation of a *Lotus japonicus* cDNA for pantothenate synthetase by functional complementation of an *E. coli panC* mutant (AT1371). A rice expressed sequence tag, identified by sequence similarity to PS, was also able to complement an *E. coli* auxotroph, as was an open reading frame from *Saccharomyces cerevisiae* (baker's yeast). The *Lotus* and rice cDNAs encode proteins of about 34 kDa which are 65% similar at the amino acid level and do not appear to encode N-terminal extensions by comparison with PS sequences from other organisms.

Figure 1 on page 673 sets forth an alignment of PS amino acid sequences from *Lotus*, rice, yeast and *E. coli* and phylogeny of known PS sequences. Percentage similarities to the lotus enzyme were 65, 56 and 46% for PS protein sequences from rice, *E. coli* and yeast respectively. It is stated on page 672, first column, that "[t]he yeast sequence is the least similar (46% identity with Lotus and *E. coli* and 41% with rice *panC*) and appears to be longer at the N-terminus by some 30 amino acids. The proteins are quite similar throughout their length, although there are two regions of greater conservation, one near the N-terminus and one in the

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middle of the protein. However, there is no clear indication of any functional significance in these regions, for example, corresponding to an ATP-binding site. . . .”

Appendix A (enclosed herewith), in Figure 1A, sets forth a comparison of pantothenate synthetase sequences from corn, eucalyptus, tulip, wheat as well as the rice and lotus sequences described in Genschel. The conserved motifs among these sequences are indicated by shading.

Thus, the information set forth in Genschel's Fig. 1 and Appendix A, could be used by one skilled in the art to understand which amino acid residues could be substituted in SEQ ID NO:9 without a likely change in function without engaging in undue experimentation. Appendix A, in Figure 1B, also presents percent identities for all the pantothenate synthetase sequences listed in Figures 1A, relative to each other. As these percent identities are all below 85%, one of ordinary skill in the art artisan would understand from the information set forth in Genschel's Fig. 1 and Appendix A the relevant, functional characteristics of the genus of sequence variants having at least 85% sequence identity to SEQ ID NO:9, and particularly which amino acids may be substituted with little functional effect.

One skilled in the art would understand that Applicants were indeed in possession of the claimed invention at the time of filing.

Claims 1-3 and 6-12 were also rejected under 35 USC §112, first paragraph, on the ground that the “specification, while being enabling for SEQ ID NO:8 and a nucleic acid sequence encoding SEQ ID NO:9, does not reasonably provide enablement for nucleic acid sequences having 85-95% sequence identity to SEQ ID NO:9 at the amino acid level. . . . Neither the state of the prior art nor Applicant provide guidance as to which regions of SEQ ID NO:8 or a sequence encoding SEQ ID NO:9 must be retained for activity, and which regions can tolerate mutations. . . .”

It is respectfully submitted that the above comments are equally apposite to this grounds of rejection.

Accordingly, withdrawal of the rejection of the claims under 35 USC §112, first paragraph, as lacking written description and lacking enablement, is respectfully requested.

It is respectfully submitted that the claims are now in condition for allowance which allowance is respectfully solicited.

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A Petition for a One (1) Month Extension of Time, Appendix A and another copy of Genschel accompany this response.

Please credit any overpayment or charge any fees that are necessary with respect to the above identified application, including but not limited to any Extension of Time, to Deposit Account No. 04-1928 (E. I. du Pont de Nemours).

Respectfully submitted,



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Appendix A

Modification of Fig. 1A & B to highlight areas of sequence identity of amino acids in pantothenate synthetases from various plants

Alignment of Pantothenate Synthetases From Corn, Eucalyptus, Soybean, Tulip, Wheat, Rice, and Lotus

SEQ ID NO:2 cpj1c.pk005.c12fis [corn]
SEQ ID NO:4 cr1n.pk0125.c12fis [corn]
SEQ ID NO:7 eej1c.pk005.p14fis [eucalyptus]
SEQ ID NO:9 ssl.pk0021.d7fis [soybean]
SEQ ID NO:11 etb1c.pk004.j20fis [tulip]
SEQ ID NO:13 wlm96.pk036.k8fis [wheat]
SEQ ID NO:14 gi2292978 [rice]
SEQ ID NO:15 gi2292921 [lotus]

1 90
SEQ ID NO:2 MAAAAA-----VHEPEVIRDKAAMRAWSRRRAEGKAVALVPTMGFLHEGHLSTLSAAVAAS-AGPIAVVVSIIYVNPSEQFAPTEDLA [corn]
SEQ ID NO:4 MAAAA-----VHEPEVIRDKAAMRAWSRRRAEGKAVALVPTMGFLHEGHLSTLSAAVAAS-AGPVAVVVSIIYVNPSEQFAPTEDLA [corn]
SEQ ID NO:7 MAAPP-----KEPLVITDKAEMREWSRRRAEQRTIALVPTMGFLHEGHLSTLVREARRADA----VVVSIVVNPSEQFAPSEDLIS [eucalyptus]
SEQ ID NO:9 MAPAP-----R---VISDKASMRWSRSMRAQKGLIGLVPTMGFLHAGHLSTVAQARQLSDV----VAVSIIYVNPSEQFAPTEDLIS [soybean]
SEQ ID NO:11 MAAPAAASSAAAAAASVSEPVIIITSKPEMLAWSRRHRRLSHTIALVPTMGSLHAGHLSTLSHAASLADLT----VVSIIYLNPTQFAPSEDLA [tulip]
SEQ ID NO:13 MAAAG-----EPEVIRDKAAMRAWSRRRAEQKTVVLVPTMGFLHEGHLSTLSAA-AAV-PGPVAVVVSIIYVNPSEQFAPTEDLA [wheat]
gi2292921 MA--P-----M---VISDKDEMCKWSRSMRSQKGLIALVPTMGFLHEGHLSTLVRDADHNHADL----VAVSIIYVNPSEQFAPTEDLIS [lotus]
gi2292978 MAAP-----REPEVIRDKAAMRAWSRRRAEQKTVAVVPTMGYLHQGHLSTLSIAAAAAASADPVAIVVTIIYVNPSEQFAPSEDLA [rice]

91 180
SEQ ID NO:2 TYP SDFAGDLRKLAAT-GVVAAVFCPPDLVVRGSA--DRPSAAGASGGAVSCLEDAGGHAHETWIRVERLEKGLICGSSRPVFFRGVATVV [corn]
SEQ ID NO:4 TYP SDFAGDLGKLAAT-GVVAAVFCPPDLVVRGSA--DRPSAASASGGAVSCLEDAGGHAHETWIRVERLEKGLICGSSRPVFFRGVATVV [corn]
SEQ ID NO:7 TYP SDFEGDLGKLRAVPGGVDFVFRPQNLVDYDQREV G-GSGVESDNGSVSCLEEK-GMGHEAWVRVERLEKMGCKSRPVFFRGVATVV [eucalyptus]
SEQ ID NO:9 TYP SDFDGDVKKLASVPGGVDVVEHPRNLYDYGNKGG-DVAEAGG--MVSCVE--SGSGHESWVRVERLEKGLICGSKSRPVFFRGVATVV [soybean]
SEQ ID NO:11 TYPADLAADLRNLRA C-PSVAAVFCPTNPY-----ADGHETWVRVERLEKGLICGLSRPVFFRGVATVV [tulip]
SEQ ID NO:13 TYP SDLAGDLRKLAAT-GAVHAVFNPPDLYHRGA AVSGRRAEAPAGAAASSCLE-AGGDGHETWIRVERLEKGLICGASRPVFFRGVATVV [wheat]
gi2292921 AYP SDFQGLDQLKLSVPGGVDVVEHPHNLYDYGGDGD-AVAECGGDVVSCVDRRSFGHETWVRAEKLEKPLCGKSRPVFFRGVATIV [lotus]
gi2292978 TYP SDFAGDLRKLAAT-GVVDVAVFNPDLVVRGA--GRRGAGS--GGAI SCLEEAAGDGHETWVRVERLEKGLICGASRPVFFRGVATIV [rice]

Figure 1A (continued)

181
SEQ ID NO:2 AKLFNIVEPDVAVFGKKDYQQWRVICRMVRDLDFAIQIVGSEVVREADGLAMSSRNVNLSSEEDRKKALSISRSLVDARTAAALSGSNR-SQ [corn]
SEQ ID NO:4 AKLFNIVEPDVAVFGKKDYQQWRVICRMVRDLDFAIQIVGSEVVREADGLAMSSRNVNLSSEEDRKKALSISRSLVDARTATLSGSNR-SQ [corn]
SEQ ID NO:7 TKLFNIVEPDVSVFGKKDYQQWRRIIRRLV-NLDFSIQIVGSEVMRDHDLGLASSRNVHLSPSEEREKALSISRSLSRAKSAAEKG-QVNCQ [eucalyptus]
SEQ ID NO:9 TKLFNIVEPDVAVFGKKDYQQWRLIQRMVRDLDFSIKVIKVGAEITRDNDGLAMSSRNVHLSPSEEREKALSINKSLRAKSAAGDG-QVHCE [soybean]
SEQ ID NO:11 SKLFHLVEPDVAVFGKKDYQQWRVIEKMVRDLDFPVRIVGSEIVREVGLAMSSRNVRLTPEEREKALSISRSLSRAKVAAQNGSSS-CQ [tulip]
SEQ ID NO:13 AKLFNVVEPDVAMFGKKDYQQWRVICRMVRDLDFAVEIIGAEIVREADGLAMSSRNVHLSPSEEREKALSISRSLNARTAAALNNSNSASE [wheat]
gi2292921 TKLFNIVEPDVAVFGKKDYQQWKIIQRMVRDLDFSIKVIKVGSEVIREKDGAMSSRNVYLSPEEREKAVSINKSLFRAKSAEEDG-QIHCE [lotus]
gi2292978 SKLFNIEPDVVPVFGKKDYQQWRVILPYWSGLDFGIEIMGSRNCARTDGLAMNSRNVHLSPSEEREKALSISRSLVDARTGALKG-NTDSK [rice]

271
SEQ ID NO:2 EIKDQIVRTITEAGGQVDYVEIVGQESLVPVERMDRPCVICVAAWFGKVRLLIDNIEIHVDSSTVLSI 325 [corn]
SEQ ID NO:4 EIKDQIVRTITEAGGQVDYVEIVEQESLVPVERMDRPCVICVAAWFGKVRLLIDNIEIHVDSSTVLSI 323 [corn]
SEQ ID NO:7 NLKDSVIOAIQIAGGKIDYAEIVDQESLEAVEEIRSPVMSCVAAWFGKVRLLIDNIEIN-----V 311 [eucalyptus]
SEQ ID NO:9 KLTNLVIOQSVTDAGGRIDYAEIVDQNNLEKVEQIKSPVFCVAAWFGKVRLLIDNMEINLS----MNV 310 [soybean]
SEQ ID NO:11 ELKDIAQOSITEAGGRIDYVEIVDQESLKVLDITSPVMCIAA WFGNVRLLIDNMEI-----TI 296 [tulip]
SEQ ID NO:13 HIKDQIVQTLTEAGGRVDYVEIVEQESLVPVETIDRPVVICVAAWFGKVRLLIDNIEIHQS----- 316 [wheat]
gi2292921 KLINLVQOSITEAGGRIDYAEIVDQNNLEKVEWIKGPVFCVSAWFGKARLLIDNIEINL----- 308 [lotus]
gi2292978 QIKNKIVQTLTETGGQVDYVEIVEQESLVPVEQIDGPVVICVAAWFGKVRLLIDNIEIDTRS----- 313 [rice]

Figure 1B

Modification of Table 4 as filed, showing a Matrix of Deduced Percent Identity for each Amino Acid Sequence in FIG. 1A and B

SID/Contig	Plant		SID2	SID4	SID7	SID9	SID11	SID13	SID15	SID14
cpj1c.pk005.c12	Corn	SID2	***	97.8	60.1	57.7	62.8	77.2	58.1	74.4
cr1n.pk0125.c12	Corn	SID4	1.9	***	60.5	57.7	61.5	77.5	58.1	74.1
eej1c.pk005.p14	Eucalyptus	SID7	45.1	44.5	***	69.4	60.8	58.8	68.8	57.2
ssl.pk0021.d7	Soybean	SID9	52.0	52.0	32.4	***	58.1	60.6	78.6	54.8
etb1c.pk004.j20	Tulip	SID11	42.7	45.0	42.7	48.7	***	61.8	56.8	56.4
wlm96.pk036.k8	Wheat	SID13	20.1	19.7	47.1	44.5	41.1	***	58.4	72.5
gi2292921	Lotus	SID15	51.8	51.8	34.8	20.8	50.3	51.8	***	54.5
gi2292978	Rice	SID14	27.3	27.3	48.7	55.9	52.5	27.5	59.0	***